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FILE 'HOME' ENTERED AT 11:31:01 ON 25 SEP 1998

=> fil caplus

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This file contains CAS Registry Numbers for easy and accurate substance identification.

This file supports REGISTRY for direct browsing and searching of all substance data from the REGISTRY file. Enter HELP FIRST for more information.

=> s amylase and active

```
      27771 AMYLASE
      4695 AMYLASES
      28456 AMYLASE
            (AMYLASE OR AMYLASES)
      497143 ACTIVE
      204 ACTIVES
      497269 ACTIVE
            (ACTIVE OR ACTIVES)
L1      1774 AMYLASE AND ACTIVE
```

=> s amylase (10a) active

```
      27771 AMYLASE
      4695 AMYLASES
      28456 AMYLASE
            (AMYLASE OR AMYLASES)
      497143 ACTIVE
      204 ACTIVES
      497269 ACTIVE
            (ACTIVE OR ACTIVES)
L2      619 AMYLASE (10A) ACTIVE
```

=> s amylase (10a) activ? (5a)residue

```
      27771 AMYLASE
      4695 AMYLASES
      28456 AMYLASE
            (AMYLASE OR AMYLASES)
      2249537 ACTIV?
      168731 RESIDUE
      212567 RESIDUES
      329369 RESIDUE
            (RESIDUE OR RESIDUES)
L3      47 AMYLASE (10A) ACTIV? (5A)RESIDUE
```

=> s l3 (10a)bacillus

```
      47106 BACILLUS
      3770 BACILLI
      136 BACILLIS
      49903 BACILLUS
            (BACILLUS OR BACILLUSES OR BACIL)
L4      3 L3 (10A)BACILLUS
```

=> d1-

D1- IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> d 1-

YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):y

L4 ANSWER 1 OF 3 CAPLUS COPYRIGHT 1998 ACS
AN 1993:97075 CAPLUS
DN 118:97075
TI Functional roles of **active site residues** of
Bacillus polymyxa .beta.-amylase
AU Uozumi, Nobuyuki
CS Fac. Eng., Nagoya Univ., Nagoya, 464-01, Japan
SO Ann. N. Y. Acad. Sci. (1992), 672(Enzyme Engineering XI), 24-8
CODEN: ANYAA9; ISSN: 0077-8923
DT Journal
LA English

L4 ANSWER 2 OF 3 CAPLUS COPYRIGHT 1998 ACS
AN 1992:250998 CAPLUS
DN 116:250998
TI Site-directed mutagenesis of **active site residues**
in **Bacillus subtilis .alpha.-amylase**
AU Takase, Kenji; Matsumoto, Takashi; Mizuno, Hiroshi; Yamane, Kunio
CS Dep. Mol. Biol., Natl. Inst. Agrobiol. Resourc., Tsukuba, Japan
SO Biochim. Biophys. Acta (1992), 1120(3), 281-8
CODEN: BBACAQ; ISSN: 0006-3002
DT Journal
LA English

L4 ANSWER 3 OF 3 CAPLUS COPYRIGHT 1998 ACS
AN 1985:127861 CAPLUS
DN 102:127861
TI An **active center tryptophan residue** in
liquefying **.alpha.-amylase** from **Bacillus**
amyloliquefaciens
AU Kochhar, Sunil; Dua, Ramji D.
CS Biochem. Lab., Indian Inst. Technol., New Delhi, 110016, India
SO Biochem. Biophys. Res. Commun. (1985), 126(2), 966-73
CODEN: BBRCA9; ISSN: 0006-291X
DT Journal
LA English

=> d 1- ab

YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):y

L4 ANSWER 1 OF 3 CAPLUS COPYRIGHT 1998 ACS
AB The effects of mutation of Cys, His, and Glu residues in conserved
regions of **.beta.-amylase** on the catalytic properties of the enzyme
are discussed.

L4 ANSWER 2 OF 3 CAPLUS COPYRIGHT 1998 ACS
AB Site-directed mutagenesis of **B. subtilis N7 .alpha.-amylase** was
performed to evaluate the roles of the active site residues in
catalysis and to prep. an inactive catalytic-site mutant that could
form a stable complex with natural substrates. Mutation of Asp-176,
Glu-208, and Asp-269 to their amide forms resulted in a >15,000-fold
redn. in its specific activity, but all of the mutants retained
considerable substrate-binding abilities as estd. by gel
electrophoresis in the presence of sol. starch. Conversion of
His-180 to Asn resulted in a 20-fold redn. in kcat with a 5-fold
increase in km for a maltopentaose deriv. The relative affinities
for acarbose vs. maltopentaose were also compared between the
mutants and wild-type enzyme. The results were consistent with the
roles previously proposed in Taka-amylase A and porcine pancreatic
.alpha.-amylase based on their x-ray crystallog. anal., although

different pairs had been assigned as catalytic residues for each enzyme. Anal. of the residual activity of the catalytic-site mutants by gel electrophoresis suggested that it derived from the wild-type enzyme contaminating the mutant prepns., which could be removed by use of an acarbose affinity column; thus, these mutants were completely devoid of activity. The affinity-purified mutant proteins should be useful for elucidating the complete picture of the interaction of this enzyme with starch.

L4 ANSWER 3 OF 3 CAPLUS COPYRIGHT 1998 ACS

AB Liquefying .alpha.-amylase from B. amyloliquefaciens was inactivated by N-bromosuccinimide. Preincubation of the enzyme with either substrate or competitive inhibitor provided significant protection against inactivation. The relation between activity loss and the no. of tryptophan residues modified, as well as presence of substrate or inhibitor in the reaction mixt., demonstrated that only 1 of 3 modifiable tryptophan residues was at or near the active center. The apparent Km of the modified enzyme for sol. starch increased substantially, thus implicating the sensitive tryptophan residue in the substrate binding region of the enzyme.

=> d 1- ab

YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):n

=> dis his

(FILE 'HOME' ENTERED AT 11:31:01 ON 25 SEP 1998)

FILE 'CAPLUS' ENTERED AT 11:32:06 ON 25 SEP 1998

L1 1774 S AMYLASE AND ACTIVE
L2 619 S AMYLASE (10A) ACTIVE
L3 47 S AMYLASE (10A) ACTIV? (5A)RESIDUE
L4 3 S L3 (10A)BACILLUS

=> amylase (15a)active center

AMYLASE IS NOT A RECOGNIZED COMMAND

The previous command name entered was not recognized by the system. For a list of commands available to you in the current file, enter "HELP COMMANDS" at an arrow prompt (=>).

=> s amylase (15a)active center

27771 AMYLASE
4695 AMYLASES
28456 AMYLASE
(AMYLASE OR AMYLASES)
497143 ACTIVE
204 ACTIVES
497269 ACTIVE
(ACTIVE OR ACTIVES)
161103 CENTER
93225 CENTERS
225957 CENTER
(CENTER OR CENTERS)
9811 ACTIVE CENTER
(ACTIVE (W) CENTER)
L5 30 AMYLASE (15A)ACTIVE CENTER

=> s 15 (15a)bacillus

47106 BACILLUS

3770 BACILLI
136 BACILLI
49903 BACILLUS

(BACILLUS OR BACILLUSES OR BACIL)

L6 4 L5 (15A) BACILLUS

=> d 1-

YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):n

=> d 16 not 14

L4 IS NOT VALID HERE

For an explanation, enter "HELP DISPLAY".

=> s 16 not 14

L7 3 L6 NOT L4

=> d 1-

YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):y

L7 ANSWER 1 OF 3 CAPLUS COPYRIGHT 1998 ACS

AN 1995:68546 CAPLUS

DN 122:26628

TI Properties and active center of the thermostable branching enzyme
from Bacillus stearothermophilus

AU Takata, Hiroki; Takaha, Takeshi; Kuriki, Takashi; Okada, Shigetaka;
Takagi, Masahiro; Imanaka, Tadayuki

CS Biochemical Research Laboratories, Ezaki Glico Co., Ltd., Osaka,
555, Japan

SO Appl. Environ. Microbiol. (1994), 60(9), 3096-104
CODEN: AEMIDF; ISSN: 0099-2240

DT Journal

LA English

L7 ANSWER 2 OF 3 CAPLUS COPYRIGHT 1998 ACS

AN 1989:547515 CAPLUS

DN 111:147515

TI Functional improvement of enzymes by recombinant DNA technology

AU Yamane, Kunio

CS Inst. Biol., Univ. Tsukuba, Tsukuba, 305, Japan

SO Gekkan Fudo Kemikaru (1989), 5(7), 31-7

CODEN: GFKEEX; ISSN: 0911-2286

DT Journal; General Review

LA Japanese

L7 ANSWER 3 OF 3 CAPLUS COPYRIGHT 1998 ACS

AN 1985:434160 CAPLUS

DN 103:34160

TI Chemical modification of liquefying .alpha.-amylase: role of
tyrosine residues at its active center

AU Kochhar, Sunil; Dua, Ramji D.

CS Biochem. Lab., Indian Inst. Technol., New Delhi, 110016, India

SO Arch. Biochem. Biophys. (1985), 240(2), 757-67

CODEN: ABBIA4; ISSN: 0003-9861

DT Journal

LA English

=> d 1- ab

YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):y

L7 ANSWER 1 OF 3 CAPLUS COPYRIGHT 1998 ACS
AB Although the branching enzyme (EC 2.4.1.18) is a member of the .alpha.-amylase family, the characteristics are not understood. The thermostable branching enzyme gene from Bacillus stearothermophilus TRBE14 was cloned and expressed in Escherichia coli. The branching enzyme was purified to homogeneity, and various enzymic properties were analyzed by the author's improved assay method. About 80% of activity was retained when the enzyme was heated at 60.degree.C for 30 min, and the optimum temp. for activity was around 50.degree.C. The enzyme was stable in the range of pH 7.5 to 9.5, and the optimum pH was 7.5. The nucleotide sequence of the gene was detd., and the active center of the enzyme was analyzed by means of site-directed mutagenesis. The catalytic residues were tentatively identified as two Asp residues and a Glu residue by comparison of the amino acid sequences of various branching enzymes from different sources and enzymes of the .alpha.-amylase family. When the Asp residues and Glu were replaced by Asn and Gln, resp., the branching enzyme activities disappeared. The results suggested that these three residues are the catalytic residues and that the catalytic mechanism of the branching enzyme is identical to that of .alpha.-amylase. On the basis of these results, four conserved regions including catalytic residues and most of the substrate-binding residues of various branching enzymes are proposed.

L7 ANSWER 2 OF 3 CAPLUS COPYRIGHT 1998 ACS
AB A review, with 15 refs., on the detn. of the **active center** and elevation of thermostability of **Bacillus .alpha.-amylase** by site-directed mutagenesis; the possibility of starch prodn. by cyclomaltodextrin gluconotransferase as a result of introducing a mutation at the active site of cyclization; and on the improvement of subtilisin activity at room temp.

L7 ANSWER 3 OF 3 CAPLUS COPYRIGHT 1998 ACS
AB Liquefying .alpha.-amylase from Bacillus amyloliquefaciens was inactivated by treatment with tetranitromethane and N-acetylimidazole. The loss of activity occurred with modification of 5 tyrosine residues. Preincubation of the enzyme with either the substrate or the competitive inhibitor at satg. levels provided complete protection against inactivation. However, the presence of substrate/inhibitor in the reaction mixt. protected only 2 of the 5 modifiable tyrosine residues, suggesting the involvement of only 2 tyrosine residues at the active center. This was confirmed when hydroxylamine treatment of the acetylated enzyme fully restored the enzymic activity. Both nitration and acetylation increased the apparent Km of the enzyme for sol. starch, which indicated that the tyrosine residues are involved in substrate binding. Redn. of nitrotyrosine residues to aminotyrosine residues failed to restore the enzymic activity. Thus, the loss of activity on modification of tyrosine residues was ascribed to conformational perturbations, and not simply to changes in the ionic character of tyrosine residues.

=> dis his

(FILE 'HOME' ENTERED AT 11:31:01 ON 25 SEP 1998)

FILE 'CAPLUS' ENTERED AT 11:32:06 ON 25 SEP 1998

L1 1774 S AMYLASE AND ACTIVE
L2 619 S AMYLASE (10A) ACTIVE
L3 47 S AMYLASE (10A) ACTIV? (5A)RESIDUE
L4 3 S L3 (10A)BACILLUS
L5 30 S AMYLASE (15A)ACTIVE CENTER

L6 4 S L5 (15A) BACILLUS
L7 3 S L6 N L4

=> log h

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
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